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10/1/02

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/642,034

DATE: 10/01/2002

TIME: 15:43:42

Input Set : A:\18501-97.app

Output Set: N:\CRF4\10012002\I642034.raw

p.6

3 <110> APPLICANT: Mack, David  
 4 Gish, Kurt C.  
 5 Eos Biotechnology, Inc.  
 7 <120> TITLE OF INVENTION: Novel Methods of Diagnosing Breast Cancer,  
 8 Compositions, and Methods of Screening for Breast  
 9 Cancer Modulators  
 11 <130> FILE REFERENCE: 018501-009700US  
 13 <140> CURRENT APPLICATION NUMBER: US 09/642,034  
 14 <141> CURRENT FILING DATE: 2000-08-18  
 16 <150> PRIOR APPLICATION NUMBER: US 09/268,865  
 17 <151> PRIOR FILING DATE: 1999-03-15  
 19 <150> PRIOR APPLICATION NUMBER: US 09/450,810  
 20 <151> PRIOR FILING DATE: 1999-11-29  
 22 <150> PRIOR APPLICATION NUMBER: US 09/453,137  
 23 <151> PRIOR FILING DATE: 1999-12-02  
 25 <150> PRIOR APPLICATION NUMBER: US 09/525,361  
 26 <151> PRIOR FILING DATE: 2000-03-15  
 28 <150> PRIOR APPLICATION NUMBER: WO PCT/US00/06952  
 29 <151> PRIOR FILING DATE: 2000-03-15  
 31 <160> NUMBER OF SEQ ID NOS: 7  
 33 <170> SOFTWARE: PatentIn Ver. 2.1  
 35 <210> SEQ ID NO: 1  
 36 <211> LENGTH: 3461  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Homo sapiens  
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 43 <220> FEATURE:  
 44 <221> NAME/KEY: CDS  
 45 <222> LOCATION: (138)..(2405)  
 46 <223> OTHER INFORMATION: human BCR4  
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 51 gcgagagacga aggcgcaatg gcgaggaagt tatctgtaat cttgatcctg acctttgccc 180  
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 53 aaattagtcc gaattgggaa tctggcatta atgttgactt ggcaatttcc acacggcaat 300  
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 59 gtaaaagatcc tagaaacagc cagggggaaag gagctcaccg accagaacat gccagtggta 660

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63 tggctggtag gaaaacaaat gaatctgtga gtgagccccg aaaaggcttt atgtattcca 900
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68 tcagtttctt gtctctgtct ggggttatct tagtgctctt catgaatcgg gtgtttttca 1200
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102 tattgccaag ttatatatca ccaaaagctg tatgactgga tgttctggtt acctggttta 3240
103 caaaattatc agagtagtaa aactttgata tatatgagga tattaact acactaagta 3300
104 tcatattgatt cgattcagaa agtactttga tatctctcag tgcctcagtg ctatcattgt 3360
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109 <210> SEQ ID NO: 2
110 <211> LENGTH: 18

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112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
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116     base sequence in BCR4 not found in published human
117     LIV-1
119 <400> SEQUENCE: 2
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125 <212> TYPE: DNA
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128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence:sequence in
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131     found in published human LIV-1
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142 <220> FEATURE:
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149 gaatctggca ttaatgttga cttggcaatt tccacacggc aatatcatct acaacagctt 180
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167 ggaccacttt tcagtcactc gtcttctcaa aacatagaag aaagtgccta ttttgattcc 1260
168 acgtggaagg gtctaacagc tctaggaggc ctgtatttca tgtttcttgt tgaacatgtc 1320
169 ctcacattga tcaaacaatt taaagataag aagaaaaaga atcagaagaa acctgaaaat 1380

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173 catgctcatc cacaggaagt ctacaatgaa tatgtacca gaggggtgcaa gaataaatgc 1620
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177 atgggtgatg gcctgcacaa tttcagcgaat ggcctagcaa ttgggtgctgc ttttactgaa 1860
178 ggcttatcaa gtggtttaag tactttctgtt gctgtgttct gtcatgagtt gcctcatgaa 1920
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182 gctctgggtg atatggtacc tgaaatgctg cacaatgatg ctagtgacca tggatgtagc 2160
183 cgctgggggt atttcttttt acagaatgct gggatgcttt tgggttttgg aattatgtta 2220
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187 &lt;210&gt; SEQ ID NO: 5

188 &lt;211&gt; LENGTH: 755

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192 &lt;220&gt; FEATURE:

193 &lt;223&gt; OTHER INFORMATION: human breast cancer protein BCR4

195 &lt;400&gt; SEQUENCE: 5

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200 Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly Ile Asn Val Asp Leu
201           35           40           45
202 Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln Leu Phe Tyr Arg Tyr
203           50           55           60
204 Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe Arg Lys Leu Leu Gln
205           65           70           75           80
206 Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His Ile His His Asp His
207           85           90           95
208 Asp His His Ser Asp His Glu His His Ser Asp His Glu Arg His Ser
209           100          105          110
210 Asp His Glu His His Ser Asp His Glu His His Ser Asp His Asp His
211           115          120          125
212 His Ser His His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala
213           130          135          140
214 Leu Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn
215           145          150          155          160
216 Ser Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg
217           165          170          175
218 Asn Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr
219           180          185          190
220 Asn Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro
221           195          200          205
222 Arg Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro

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| 225 | 225   | 230 | 235 |
| 226 | Asn Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn |     | 240 |
| 227 |   | 245 | 250 |
| 228 | Thr Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr |     | 255 |
| 229 |   | 260 | 265 |
| 230 | Ser His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn |     | 270 |
| 231 |   | 275 | 280 |
| 232 | Tyr Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu |     | 285 |
| 233 |   | 290 | 295 |
| 234 | Ile His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser |     | 300 |
| 235 | 305   | 310 | 315 |
| 236 | Leu Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser |     | 320 |
| 237 |   | 325 | 330 |
| 238 | Phe Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val |     | 335 |
| 239 |   | 340 | 345 |
| 240 | Phe Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr |     | 350 |
| 241 |   | 355 | 360 |
| 242 | Leu Ser Gly Asp Ala Phe Leu His Leu Leu Pro His Ser His Ala Ser |     | 365 |
| 243 |   | 370 | 375 |
| 244 | His His His Ser His Ser His Glu Glu Pro Ala Met Glu Met Lys Arg |     | 380 |
| 245 | 385   | 390 | 395 |
| 246 | Gly Pro Leu Phe Ser His Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala |     | 400 |
| 247 |   | 405 | 410 |
| 248 | Tyr Phe Asp Ser Thr Trp Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr |     | 415 |
| 249 |   | 420 | 425 |
| 250 | Phe Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys |     | 430 |
| 251 |   | 435 | 440 |
| 252 | Asp Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val |     | 445 |
| 253 |   | 450 | 455 |
| 254 | Glu Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn |     | 460 |
| 255 | 465   | 470 | 475 |
| 256 | Glu Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala |     | 480 |
| 257 |   | 485 | 490 |
| 258 | Asp Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu |     | 495 |
| 259 |   | 500 | 505 |
| 260 | Glu Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr |     | 510 |
| 261 |   | 515 | 520 |
| 262 | Asn Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe |     | 525 |
| 263 |   | 530 | 535 |
| 264 | His Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His Asp     |     | 540 |
| 265 | 545   | 550 | 555 |
| 266 | Tyr His His Ile Leu His His His His His Gln Asn His His Pro His |     | 560 |
| 267 |   | 565 | 570 |
| 268 | Ser His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val |     | 575 |
| 269 |   | 580 | 585 |
| 270 | Ala Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe |     | 590 |
| 271 |   | 595 | 600 |
|     |   |     | 605 |

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 3